



Full wwPDB X-ray Structure Validation Report ⓘ

May 3, 2016 – 02:45 PM EDT

PDB ID : 5BST
Title : Crystal structure of 4-coumarate:CoA ligase complexed with coumaroyl adenylate
Authors : Li, Z.; Nair, S.K.
Deposited on : 2015-06-02
Resolution : 1.61 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027457
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

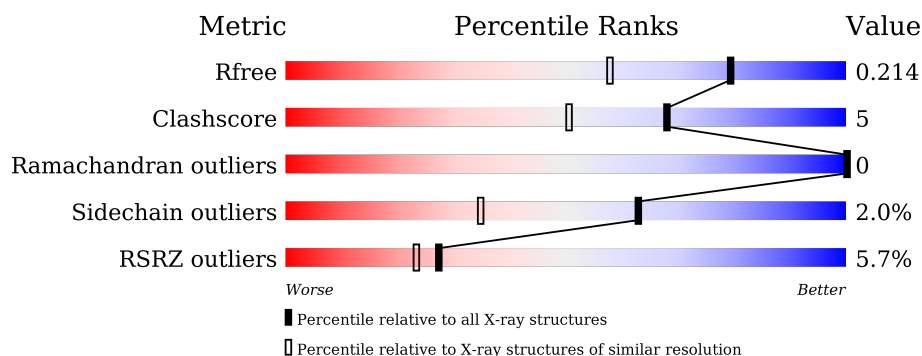
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.61 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3202 (1.64-1.60)
Clashscore	102246	3500 (1.64-1.60)
Ramachandran outliers	100387	3411 (1.64-1.60)
Sidechain outliers	100360	3410 (1.64-1.60)
RSRZ outliers	91569	3207 (1.64-1.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	542	<div> <div>6%</div> <div>88%</div> <div>9% ..</div> </div>

2 Entry composition [i](#)

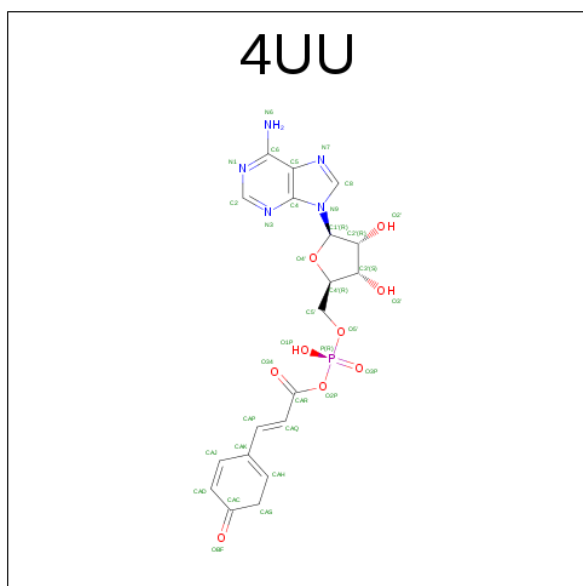
There are 4 unique types of molecules in this entry. The entry contains 4618 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 4-coumarate–CoA ligase 2.

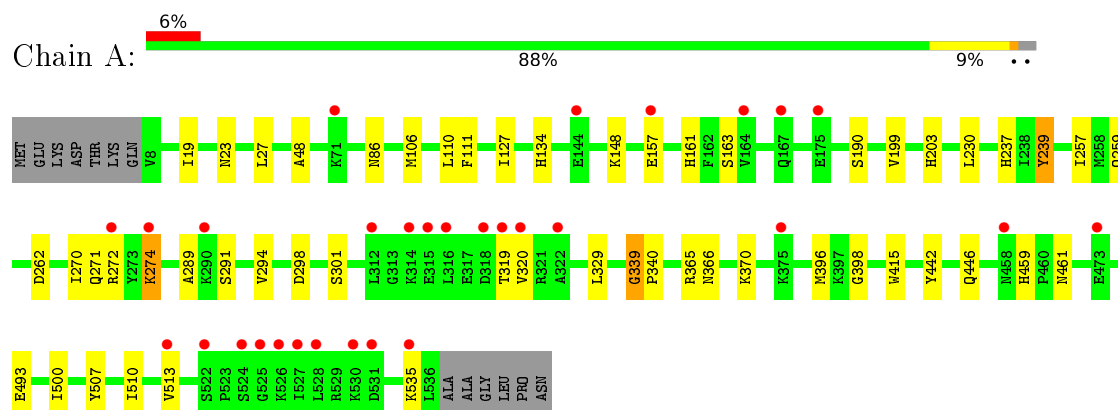
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	529	Total	C	N	O	S	0	0	0
			4080	2618	676	764	22			

- Molecule 2 is 5'-O-[(R)-hydroxy{[(2E)-3-(4-oxocyclohexa-1,5-dien-1-yl)prop-2-enoyl]oxy}phosphoryl]adenosine (three-letter code: 4UU) (formula: C₁₉H₂₀N₅O₉P).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	503	Total 503	O 503	0	0

- Molecule 1: 4-coumarate–CoA ligase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	81.83Å 81.83Å 180.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 1.61 39.91 – 1.61	Depositor EDS
% Data completeness (in resolution range)	99.0 (25.00-1.61) 99.1 (39.91-1.61)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.38 (at 1.61Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.199 , 0.215 0.199 , 0.214	Depositor DCC
R_{free} test set	3988 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	15.2	Xtriage
Anisotropy	0.350	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 39.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4618	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 4UU

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.29	0/4164	0.53	1/5651 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	339	GLY	N-CA-C	5.19	126.08	113.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4080	0	4147	39	0
2	A	34	0	0	1	0
3	A	1	0	0	0	0
4	A	503	0	0	5	1
All	All	4618	0	4147	39	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (39) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:VAL:HG13	1:A:396:MET:HE3	1.28	1.15
1:A:27:LEU:H	1:A:203:HIS:HD2	1.07	0.95
1:A:271:GLN:HE21	1:A:298:ASP:H	1.21	0.86
1:A:19:ILE:H	1:A:366:ASN:HD21	1.20	0.85
1:A:27:LEU:H	1:A:203:HIS:CD2	1.98	0.78
1:A:199:VAL:CG1	1:A:396:MET:HE3	2.09	0.78
1:A:199:VAL:HG13	1:A:396:MET:CE	2.15	0.72
1:A:459:HIS:HD2	1:A:461:ASN:H	1.39	0.69
1:A:271:GLN:NE2	1:A:298:ASP:H	1.89	0.68
1:A:396:MET:HE2	1:A:398:GLY:O	1.96	0.65
1:A:134:HIS:HD2	4:A:750:HOH:O	1.78	0.65
1:A:500:ILE:HG13	1:A:510:ILE:HD12	1.81	0.62
1:A:199:VAL:HA	1:A:396:MET:HE1	1.83	0.60
1:A:274:LYS:HD2	4:A:825:HOH:O	2.03	0.58
1:A:446:GLN:NE2	4:A:701:HOH:O	2.36	0.58
1:A:339:GLY:N	1:A:340:PRO:HA	2.19	0.58
1:A:86:ASN:HB3	1:A:257:ILE:HG23	1.87	0.57
1:A:157:GLU:HG2	4:A:1020:HOH:O	2.05	0.57
1:A:237:HIS:HE1	2:A:601:4UU:O3P	1.88	0.55
1:A:161:HIS:CD2	1:A:163:SER:H	2.26	0.54
1:A:274:LYS:HG2	1:A:301:SER:HB3	1.89	0.54
1:A:365:ARG:HG3	1:A:366:ASN:HD22	1.72	0.54
1:A:396:MET:CE	1:A:398:GLY:O	2.56	0.53
1:A:48:ALA:HB2	1:A:259:GLN:OE1	2.10	0.52
1:A:203:HIS:HE1	4:A:731:HOH:O	1.94	0.50
1:A:274:LYS:HD3	1:A:301:SER:HB2	1.94	0.50
1:A:493:GLU:HG3	1:A:513:VAL:HG22	1.95	0.49
1:A:230:LEU:HD22	1:A:270:ILE:HD11	1.94	0.48
1:A:237:HIS:CD2	1:A:239:TYR:H	2.31	0.48
1:A:190:SER:H	1:A:446:GLN:HE22	1.62	0.48
1:A:493:GLU:HA	1:A:513:VAL:HG21	1.97	0.46
1:A:291:SER:HB2	1:A:294:VAL:HG23	1.98	0.46
1:A:161:HIS:HD2	1:A:163:SER:H	1.64	0.44
1:A:370:LYS:HE2	1:A:415:TRP:CD2	2.53	0.44
1:A:199:VAL:HA	1:A:396:MET:CE	2.47	0.44
1:A:127:ILE:HG12	1:A:148:LYS:HB2	2.00	0.42
1:A:320:VAL:HB	1:A:329:LEU:HD22	2.01	0.41
1:A:289:ALA:HB2	1:A:319:THR:HG21	2.03	0.40
1:A:442:TYR:CD2	1:A:507:TYR:HB2	2.56	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:884:HOH:O	4:A:884:HOH:O[7_555]	2.00	0.20

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	527/542 (97%)	514 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	452/463 (98%)	443 (98%)	9 (2%)	63	35

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
1	A	106	MET
1	A	110	LEU
1	A	111	PHE
1	A	239	TYR
1	A	262	ASP

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Mol	Chain	Res	Type
1	A	272	ARG
1	A	274	LYS
1	A	535	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
1	A	134	HIS
1	A	161	HIS
1	A	167	GLN
1	A	203	HIS
1	A	237	HIS
1	A	271	GLN
1	A	366	ASN
1	A	446	GLN
1	A	459	HIS
1	A	474	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length

(or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	4UU	A	601	-	34,37,37	2.01	6 (17%)	32,54,54	2.28	6 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	4UU	A	601	-	-	0/14/46/46	0/4/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	4UU	CAS-CAH	-5.38	1.39	1.49
2	A	601	4UU	CAD-CAC	-2.77	1.40	1.45
2	A	601	4UU	OBf-CAC	2.02	1.26	1.23
2	A	601	4UU	CAD-CAJ	2.08	1.40	1.35
2	A	601	4UU	CAH-CAK	4.91	1.39	1.34
2	A	601	4UU	O2P-CAR	7.36	1.45	1.37

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	4UU	N3-C2-N1	-9.95	121.05	128.87
2	A	601	4UU	O2P-CAR-O34	-2.98	119.67	122.20
2	A	601	4UU	CAQ-CAP-CAK	-2.44	122.25	126.29
2	A	601	4UU	CAJ-CAD-CAC	-2.19	119.77	121.97
2	A	601	4UU	O2P-CAR-CAQ	2.95	117.78	110.91
2	A	601	4UU	CAS-CAC-CAD	3.22	120.00	115.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	4UU	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	529/542 (97%)	0.09	30 (5%)	27 23	8, 15, 31, 51	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	525	GLY	7.3
1	A	315	GLU	5.9
1	A	319	THR	5.7
1	A	320	VAL	5.6
1	A	524	SER	4.2
1	A	316	LEU	3.6
1	A	528	LEU	3.5
1	A	314	LYS	3.3
1	A	375	LYS	3.2
1	A	522	SER	3.1
1	A	157	GLU	3.0
1	A	274	LYS	3.0
1	A	473	GLU	3.0
1	A	164	VAL	2.9
1	A	530	LYS	2.7
1	A	527	ILE	2.6
1	A	458	ASN	2.6
1	A	318	ASP	2.5
1	A	144	GLU	2.5
1	A	272	ARG	2.5
1	A	175	GLU	2.4
1	A	290	LYS	2.4
1	A	167	GLN	2.4
1	A	535	LYS	2.4
1	A	531	ASP	2.4
1	A	526	LYS	2.3
1	A	312	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	71	LYS	2.2
1	A	322	ALA	2.2
1	A	513	VAL	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	MG	A	602	1/1	0.98	0.12	-0.15	9,9,9,9	0
2	4UU	A	601	34/34	0.97	0.07	-0.81	9,10,10,10	0

6.5 Other polymers [i](#)

There are no such residues in this entry.